

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti  
Corley, Neil C.  
Patterson, Chandra
- (ii) TITLE OF THE INVENTION: HUMAN NEUROSECRETORY PROTEINS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Dr.
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Cerrone, Michael C.
  - (B) REGISTRATION NUMBER: 39,132
  - (C) REFERENCE/DOCKET NUMBER: PF-0510 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 468 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: ISLTNOT01
  - (B) CLONE: 2379427
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu Pro  
 1 5 10 15  
 Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser Leu His  
 20 25 30  
 Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln Ile Ala Glu  
 35 40 45  
  
 Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro Glu Asn Lys Pro  
 50 55 60  
 Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu Asn Leu Leu Lys Ala  
 65 70 75 80  
 Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu Arg Gln Ser Ile Arg Ser  
 85 90 95  
 Ser Pro Leu Asp Asn Lys Leu Asn Val Glu Asp Val Asp Ser Thr Lys  
 100 105 110  
 Asn Arg Lys Leu Ile Asp Asp Tyr Asp Ser Thr Lys Ser Gly Leu Asp  
 115 120 125  
 His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu Asp Gly Thr  
 130 135 140  
 Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Ala Arg Ile Tyr  
 145 150 155 160  
 Glu Glu Asn Asp Arg Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu  
 165 170 175  
 Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu  
 180 185 190  
 Val Ala Glu Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr  
 195 200 205  
 Glu Glu Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly  
 210 215 220  
 Lys Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu  
 225 230 235 240  
 Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu Thr  
 245 250 255  
 Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn Phe Glu  
 260 265 270  
 Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys Ser Ile Asp  
 275 280 285  
 Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr Ile Met Lys  
 290 295 300  
 Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly Thr Ile Ser  
 305 310 315 320  
 Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu Met Ile Ala  
 325 330 335  
 Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Ala Thr Asp Asn Ile Ser  
 340 345 350  
 Lys Leu Phe Pro Ala Pro Ser Glu Lys Ser His Glu Glu Thr Asp Ser  
 355 360 365  
 Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly Ser Leu Lys  
 370 375 380  
 Asp Ser Thr Lys Asp Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu  
 385 390 395 400  
 Pro Lys Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile  
 405 410 415  
 Glu Trp Leu Lys Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp  
 420 425 430  
 Leu Ser Lys Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val  
 435 440 445  
 Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile  
 450 455 460

Tyr Ser Ser Leu  
465

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: ISL1NOT01
- (B) CLONE: 2379427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGCGCTCCC	CTCTACCTGG	AGACTTGACT	CCCGCGCCGC	CCAACCCCTGC	TTATCCCTTG	60
ACCGTGGAGT	CTCAGAGATC	CTGCAGCCGC	CCAGTCCCGG	CCCCCTCTCC	GCCCCACACC	120
CACCGCTCTG	GCTCTTCTCG	TTTTTACTCC	TCCTTTTTCAT	TCATAACAAA	AGCTACAGCT	180
CCAGGAGGCC	AGCGCCGGGC	TGTGACCCAA	GCGAGCGCTG	GAAGAATGGG	GTTCCGCGGG	240
ACCGGCACCT	GGATTCTGGT	GTTAGTGCTC	CCGATTCAAG	CTTTCCCCAA	ACCTGGAGGA	300
AGCCCAAGAA	AATCTCTACA	TAATAGAGAA	TTAAGTGCAG	AAAGACCTTT	GAATGAAGAG	360
ATTGCTGAAG	CAGAAGAAGA	CAAGATTAAA	AAAACATATC	CTCCAGAAAA	CAAGCCAGGT	420
CAGAGCAACT	ATTCTTTTGT	TGATAACTTG	AACCTGCTAA	AGGCAATAAG	AGAAAAGGAA	480
AAAATTGAGA	AAGAAAGACA	ATCTATAAGA	AGCTCCCCAC	TTGATAATAA	GTTGAATGTG	540
GAAGATGTTG	ATTCAACCAA	GAATCGAAAA	CTGATCGATG	ATTATGACTC	TACTAAGAGT	600
GGATTGGATG	ATAAATTTC	AGATGATCCA	GATGGTCTTC	ATCACTAGAG	CGGGAAGGAG	660
TTAACCGCTG	AAGACATTTG	CCATATAAATC	GCTGCCAGGA	TTTATGAAGA	AAATGACAGA	720
GCCGTGTTTG	ACAAGATTGT	TTCTAAACTA	CTTAATCTCG	GCCTTATCAC	AGAAAGCCAA	780
GCACATACAC	TGGAAGATGA	AGTAGCAGAG	GTTTTACAAA	AATTAATCTC	AAAGGAAGCC	840
AACAATTATG	AGGAGGATCC	CAATAAGCCC	ACAAGCTGGA	CTGAGAATCA	GGCTGGAAAA	900
ATACCAGAGA	AAGTGACTCC	AATGGCAGCA	ATTCAAGATG	GTCTTGCTAA	GGGAGAAAAAC	960
GATGAAACAG	TATCTAACAC	ATTAACTCTG	ACAAATGGCT	TGGAAAGGAG	AACTAAAAAC	1020
TACAGTGAAG	ACAACCTTGA	GGAACTCCAA	TATTTCCCAA	ATTCTATATG	GCTACTGAAA	1080
AGTATTGATT	CAGAAAAAGA	AGCAAAAGAG	AAAGAAACAC	TGATTACTAT	CATGAAAAACA	1140
CTGATTGACT	TTGTGAAGAT	GATGGTGAAA	TATGGAACAA	TATCTCCAGA	AGAGGATGTT	1200
TCCTACTCTG	AAAACCTTGA	TGAAATGATT	GCTCTTCAGA	CCAAAAACAA	GCTAGAAAAAA	1260
AATGCTACTG	ACAATATAAG	CAAGCTTTTC	CCAGCACCAT	CAGAGAAAGG	TCATGAAGAA	1320
ACAGACAGTA	CCAAGGAAGA	AGCAGCTAAG	ATGGAAGGAG	AATATGGAAG	CTTGAAGGAT	1380
TCCACAAAAA	ACGATTAATC	CAACCCAGGA	GGAAGAGCAG	ATGAACCCAA	AGGAAAAACA	1440
GAAGCCTATT	TGGAAGCCAT	CAGAAAAAAT	ATTGAATGGT	TGAAGAAAAA	TGACAAAAAG	1500
GGAAATTAAG	AAGATTATGA	CCTTTCAAAG	ATGAGAGACT	TCATCAATAA	ACAAGCTGAT	1560
GCTTATGTGG	AGAAAGGCAT	CCTTGACAAG	GAAGAAGCCG	AGGCCATCTA	GCGCATTTTAT	1620
AGCAGCGCTG	AAAAATGGCA	AAAGATCCAG	GAGTCTTTCA	ACTGTTTCAG	AAAAACATAAT	1680
ATAGCTTAAA	ACACTTTCTA	TTCTGTGATT	AAAAATTTT	GACCCAAAGG	TTATTAGAAA	1740
GTGCTGAATT	TACAGTAGTT	AACCTTTTAC	AAATGGTTAA	AACATAGCTT	TCTTCCCGTA	1800
AAAACATATC	GAAAGTAAAG	TTGATGTGTA	GCTGAAAAAA	AAAA		1844

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT14

PF-0510 US

(B) CLONE: 2744187

1007040 02140  
201120 010700

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala  
 1 5 10 15  
 Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser  
 20 25 30  
 Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro  
 35 40 45  
 Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu  
 50 55 60  
 Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro  
 65 70 75 80  
 Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser  
 85 90 95  
 Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr  
 100 105 110  
 Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr  
 115 120 125  
 Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro  
 130 135 140  
 Ser Lys Ile Gln Leu Pro Glu Asp Glu  
 145 150

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRSTTUT14  
 (B) CLONE: 2744187

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGCCGCTGG CTCCGTTTCA CTTCCACGCC ACCCCCGCTG CTGCTACCAT GATCTGCCAG 60  
 CCTGGGTGAT GCTTCTTGCA GGGACTCTTC TCGGCCCGGG CTGTCAAGGA AGGGCTCCCA 120  
 GACATCACCT CTGCCCGCCG CCACCTCTTC CAACTCTCCC AGCTCAGCCG GAGCCGGAGC 180  
 GCGCAACAAC CAAGTCCGAG ACTGGAGGCA GATCGGGGGG AGGGGAGAAG CGCCAAGCGC 240  
 GCTGCCCTCC CAGGGAAACT CACTGCCGCC TACTCCAGC CGGCCACAGT ACCAGCTCA 300  
 AAATGCGGAC GACGAGAAGG GAGTCGGCGC TCCGACCACC ATCCACCTAC TAAGGAAGCG 360  
 CGCTCTGGCC GCGCCCGCGC ATTGGTCACC GCGCGCTAGG GGACAGCCCT GGCCTCTCTCT 420  
 GATTGGCAAG CGCTGGCCAC CTCCCACAC CCCTTGCAGG CGCTCCCTTA GTGGAGAAAA 480  
 GGAGTAGCTA TTAGCCAATT CGGGCAGGGC CGCTTTTITA GAAGCTTGAT TTCTTTTGAA 540  
 GATGAAGAAG TAGCGAAGC TCTGCCTCTT TCCCCAGTGG GCGAGGGAAC TCGGGCGCAT 600  
 TGGCTGGGAA CTGTATCCAC CAAATGTCAC CGATCTCTCC TATGCAAGGA ATGAGCAGAC 660  
 CCATCAATAA GAAATTTCTC AGCCTGGCCG AAAATGGTTG GCCCCACGAA GCCACGACAA 720  
 CTGGAGGCAG AGAGGGTTGC TCAACGCCCC GCCTCATTGG AAAACCAAAAT CAGATCTGGG 780  
 ACCATATATG CGTGGCGGAG GCGGGCGGAT GATTGTGCGG CTGCACCCA CTGAGCTGTC 840  
 GCACAGTGCG ATTTCTTTTC CCGCCCTTGA GACCCCTGCA CACCATCTGT CATGGCGGCT 900  
 GGGCTGTGTT GTTTGAGCGC TCGCCGTCTT TTGGCGGCAG CGCGGACGCG CATGCTCCCG 960  
 GCGCCCGCGG TCCGCTGGGA ATCTAGCTTC TCCAGGACTG TGGTCCGCCCC GTCGCTGTG 1020  
 GCGGGAAGAC GGCCCCCAGA ACCGACCACA CCGTGGCAAG AGGACCCAGA ACCCGAGGAC 1080  
 GAAAATCTGT ATGAGAAGAA CCCAGACTCC CATGGTTATG ACAAGGACCC CGTTTTGGAC 1140  
 GTCTGAACA TCGCACTTGT TCTTCTTTT GCGCTTCCA TCATCTGTGT CAGCTCCAGC 1200  
 ACCTTTGTGG CCTATCTGCC TGACTACAGG ATGAAAGAGT GGTCCCGCCG CGAAGCTGAG 1260

AGGCTTGTTGA	AATACCGAGA	GGCCAATGGC	CTTCCCATCA	TGGAATCCAA	CTGCTTCGAC	1320
CCCAGCAAGA	TCCAGCTGCC	AGAGGATGAG	TGACCAGTTG	CTAAGTGGGG	CTCAAGAAGC	1380
ACCGCTTCC	CCACCCCTCG	CTGCCATTC	TGACCTCTTC	TCAGAGCACC	TAATTAAAGG	1440
GGCTGAAAGT	CTGAAAAAAA	AAA				1463

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 413764

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Gly	Phe	Leu	Trp	Thr	Gly	Ser	Trp	Ile	Leu	Val	Leu	Val	Leu	Asn	
1				5					10					15		
Ser	Gly	Pro	Ile	Gln	Ala	Phe	Pro	Lys	Pro	Glu	Gly	Ser	Gln	Asp	Lys	
			20					25					30			
Ser	Leu	His	Asn	Arg	Glu	Leu	Ser	Ala	Glu	Arg	Pro	Leu	Asn	Glu	Gln	
		35					40					45				
Ile	Ala	Glu	Ala	Glu	Ala	Asp	Lys	Ile	Lys	Lys	Ala	Phe	Pro	Ser	Glu	
	50					55					60					
Ser	Lys	Pro	Ser	Glu	Ser	Asn	Tyr	Ser	Ser	Val	Asp	Asn	Leu	Asn	Leu	
65				70						75				80		
Leu	Arg	Ala	Ile	Thr	Glu	Lys	Glu	Thr	Val	Glu	Lys	Glu	Arg	Gln	Ser	
			85						90				95			
Ile	Arg	Ser	Pro	Pro	Phe	Asp	Asn	Gln	Leu	Asn	Val	Glu	Asp	Ala	Asp	
			100					105					110			
Ser	Thr	Lys	Asn	Arg	Lys	Leu	Ile	Asp	Glu	Tyr	Asp	Ser	Thr	Lys	Ser	
		115				120					125					
Gly	Leu	Asp	His	Lys	Phe	Gln	Asp	Asp	Pro	Asp	Gly	Leu	His	Gln	Leu	
	130					135					140					
Asp	Gly	Thr	Pro	Leu	Thr	Ala	Glu	Asp	Ile	Val	His	Lys	Ile	Ala	Thr	
145				150						155					160	
Arg	Ile	Tyr	Glu	Glu	Asn	Asp	Arg	Gly	Val	Phe	Asp	Lys	Ile	Val	Ser	
			165							170				175		
Lys	Leu	Leu	Asn	Leu	Gly	Leu	Ile	Thr	Glu	Ser	Gln	Ala	His	Thr	Leu	
	180						185						190			
Glu	Asp	Glu	Val	Ala	Glu	Ala	Leu	Gln	Lys	Leu	Ile	Ser	Lys	Glu	Ala	
	195					200					205					
Asn	Asn	Tyr	Glu	Glu	Thr	Leu	Asp	Lys	Pro	Thr	Ser	Arg	Thr	Glu	Asn	
	210				215						220					
Gln	Asp	Gly	Lys	Ile	Pro	Glu	Lys	Val	Thr	Pro	Val	Ala	Ala	Val	Gln	
225					230					235					240	
Asp	Gly	Phe	Thr	Asn	Arg	Glu	Asn	Asp	Glu	Thr	Val	Ser	Asn	Thr	Leu	
			245						250				255			
Thr	Leu	Ser	Asn	Gly	Leu	Glu	Arg	Arg	Thr	Asn	Pro	His	Arg	Glu	Asp	
	260						265						270			
Asp	Phe	Glu	Glu	Leu	Gln	Tyr	Phe	Pro	Asn	Phe	Tyr	Ala	Leu	Leu	Thr	
	275						280					285				
Ser	Ile	Asp	Ser	Glu	Lys	Glu	Ala	Lys	Glu	Lys	Glu	Thr	Leu	Ile	Thr	
	290				295						300					
Ile	Met	Lys	Thr	Leu	Ile	Asp	Phe	Val	Lys	Met	Met	Val	Lys	Tyr	Gly	
305				310						315					320	

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Thr Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu
      325                      330
Thr Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Thr Thr Asp
      340                      345                      350
Ser Lys Ser Lys Leu Phe Pro Ala Pro Pro Glu Lys Ser Gln Glu Glu
      355                      360                      365
Thr Asp Ser Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly
      370                      375                      380
Ser Leu Lys Asp Ser Thr Lys Asp Asp Asn Ser Asn Leu Gly Gly Lys
      385                      390                      395                      400
Thr Asp Glu Ala Thr Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg
      405                      410                      415
Lys Asn Ile Glu Trp Leu Lys Lys His Asn Lys Lys Gly Asn Lys Glu
      420                      425                      430
Asp Tyr Asp Leu Ser Lys Met Arg Asp Phe Ile Asn Gln Gln Ala Asp
      435                      440                      445
Ala Tyr Val Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Asn Ala Ile
      450                      455                      460
Lys Arg Ile Tyr Ser Ser Leu
      465                      470

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## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank  
 (B) CLONE: 1771306

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser Arg Ala
  1           5           10           15
Val Ile Ala Pro Ser Gly Val Glu Lys Arg Gln Arg Glu Pro Thr
      20           25           30
Met Gln Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu Asn Val Tyr Ala
      35           40           45
Lys Asn Pro Asp Phe His Gly Tyr Asp Ser Asp Pro Val Val Asp Val
      50           55           60
Trp Asn Met Arg Ala Val Phe Phe Phe Gly Phe Ser Ile Val Leu Val
      65           70           75           80
Phe Gly Thr Thr Phe Val Ala Tyr Val Pro Asp Tyr Arg Met Gln Glu
      85           90           95
Trp Ala Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Val Asn
      100          105          110
Gly Leu Pro Ile Met Glu Ser Asn Tyr Phe Asp Pro Ser Lys Ile Gln
      115          120          125
Leu Pro Glu Asp Asp
      130

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